

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:09:22 ; Search time 124.164 Seconds
(without alignments)
1102.679 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*)
7: geneseqp2003bs:*
8: geneseqp2004s:*

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:22:29 ; Search time 27.4746 Seconds
(without alignments)
1239.716 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:10:36 ; Search time 123.636 Seconds
(without alignments)
1466.210 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:09:22 ; Search time 110.836 Seconds
(without alignments)
1102.679 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:22:29 ; Search time 24.5254 Seconds
(without alignments)
1239.716 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:10:36 ; Search time 110.364 Seconds
(without alignments)
1466.210 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

OM protein - protein search, using sw model

Run on: August 3, 2005, 14:59:46 ; Search time 32.2299 Seconds
(without alignments)
819.916 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:08:42 ; Search time 113.597 Seconds
(without alignments)
1214.127 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:02:41 ; Search time 373.021 Seconds
(without alignments)
1108.448 Million cell updates/sec

Title: US-10-670-863-1
Perfect score: 1927
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIYQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
 17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
 18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
 19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
 24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
 26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
 32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
 33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
 34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
 35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
 36: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
 37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:05:27 ; Search time 47.5522 Seconds
 (without alignments)
 1072.555 Million cell updates/sec

Title: US-10-670-863-1
 Perfect score: 1927
 Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIYQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 664618 seqs, 144074520 residues

Total number of hits satisfying chosen parameters: 664618

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_New:*
 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 14:59:46 ; Search time 28.7701 Seconds
(without alignments)
819.916 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:08:42 ; Search time 101.403 Seconds
(without alignments)
1214.127 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: *
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep: *
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep: *
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep: *
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep: *
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep: *
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep: *
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep: *
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: *

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:02:41 ; Search time 332.979 Seconds
(without alignments)
1108.448 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
Perfect score: 1712
Sequence: 1 MTAKPLRTVLSSLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep: *
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep: *
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep: *
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep: *
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep: *
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep: *
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep: *
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep: *
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep: *
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep: *
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep: *
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep: *
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep: *
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep: *
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep: *
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep: *
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep: *

20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
 24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
 26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
 32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
 33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
 34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
 35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
 36: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
 37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:05:27 ; Search time 42.4478 Seconds
 (without alignments)
 1072.555 Million cell updates/sec

Title: US-10-670-863-1_COPY_1_316
 Perfect score: 1712
 Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 664618 seqs, 144074520 residues

Total number of hits satisfying chosen parameters: 664618

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending Patents_AA New:*
 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:22:19 ; Search time 294.332 Seconds
 (without alignments)